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AMENDMENT TO THE SPECIFICATION

Please replace the first paragraph on page 5, lines 10-23, with the following amended paragraph:

This invention is directed to methods for determining the amino acid sequence of a polypeptide using mass spectrometry of differentially labeled polypeptides. The methods of the invention are applicable to proteome analysis of complex mixtures and allow rapid and efficient determination of the sequence of a polypeptide in a sample. The methods are based on comparisons of mass spectra from polypeptide samples or mixtures that have been labeled differentially according to mass. One advantage of the methods of the invention is that mass spectra data of differentially labeled polypeptide samples deposited in databases can be analyzed to determine, de novo, a particular polypeptide polypeptide amino acid sequence.